AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1-19 (canceled)

20. (previously presented) A method for the identification of populations or breeds of ruminant mammals such as cattle, sheep and goats, said method being carried out starting with a biological sample collected from the animal, in particular starting with sperm, embryo, blood, milk, hairs, carcass or meat, or other products derived from the latter, and making it possible to check, or even to certify, whether or not the animal from which said biological sample was collected belongs to a population or breed of ruminant mammals, this method comprising:

- a stage of amplification of the number of copies of the different allelic forms of the *SILVER* gene, namely of the *SI*, and/or *si*, and/or si_1 alleles, and/or of fragments of these allelic forms, specific to a population or breed of specific ruminant mammals, and capable of being present in said biological sample,

- a stage of detection of said allelic forms or fragments of the latter.

21. (currently amended) The method ~~of~~ according to claim ~~21~~ 20, wherein the method is for the identification of different cattle populations or breeds, or of different cattle herds each including several cattle populations or breeds, ~~comprising~~ and comprises a stage of amplification of the number of copies of the different allelic forms of the *SILVER* gene represented by SEQ ID NO: 1, coding for the bovine SI protein represented by SEQ ID NO: 2, and/or of fragments of this gene represented by SEQ ID NO: 1 or of its different allelic forms.

22. (currently amended) The method according to claim 20, ~~making it possible~~ wherein said method is able to check, or even to certify, that an animal belongs to a particular cattle population or breed, or to a particular cattle herd, or, on the other hand, making it possible to certify the exclusion of this animal from this population or breed, or from this particular herd.

23. (currently amended) The method according to claim 20, ~~characterized in that~~ wherein cattle populations or breeds or cattle herds are of French origin.

24. (previously presented) The method according to claim 20, comprising the amplification:

- of the nucleotide sequence corresponding to the *si* allelic form represented by SEQ ID NO: 3, coding for the bovine si protein represented by SEQ ID NO: 4, or corresponding to fragments of this allelic form, said allelic form comprising the G93A mutation with respect to the *SI* gene, said method making it possible to check, or even to certify, that an animal belongs to the Charolais breed,

- of the nucleotide sequence corresponding to the si_1 allelic form, represented by SEQ ID NO: 5, coding for the bovine si_1 protein represented by SEQ ID NO: 6, or corresponding to fragments of this allelic form, said allelic form comprising a deletion of the three nucleotides TTC situated in positions 82, 83 and 84 with respect to the *SI* gene, said method making it possible to check, or even to certify, that an animal belongs to the Simmental breed,

- of the nucleotide sequence corresponding to the bovine *SI* gene represented by SEQ ID NO: 1, or to fragments of this gene, said method making it possible to certify the exclusion of an animal from the Charolais breed.

25. (currently amended) The method ~~of~~ according to claim 20, comprising the amplification of fragments of the nucleotide sequences corresponding to the allelic forms, *SI*, *si*, and si_1, represented by SEQ ID NO: 1, 3, and 5 respectively, said fragments being chosen from those of approximately 10 to 300

nucleotides containing the nucleotides situated in positions 82 to 93 of said sequences.

26.(currently amended) The method ~~of~~ according to claim 20, comprising the amplification of fragments of the nucleotide sequences corresponding to the allelic forms *SI*, *si*, and si_1, said fragments being chosen from those of 294 nucleotides delimited by the nucleotides situated in positions 9 and 302 of the sequences SEQ ID NO: 1 and 3, these fragments being represented by the sequences SEQ ID NO: 7, and SEQ ID NO: 8 respectively, and the fragment of 291 nucleotides delimited by the nucleotides situated in positions 9 and 299 of the sequence SEQ ID NO: 5, this fragment being represented by the sequence SEQ ID NO: 9.

27. (currently amended) The method ~~of~~ according to claim 20, comprising the amplification by nucleotide primers of the number of copies of the *SILVER* gene, or of the different allelic forms of this gene, or of the fragments of this gene or of its different allelic forms.

28. (previously presented) The method of claim 20, comprising the amplification by nucleotide primers of the number of copies of the *SILVER* gene, or of the different allelic forms of this gene, or of the fragments of this gene or of its

different allelic forms, wherein said nucleotide primers are in the form of 5'-3' primer pairs, these pairs being such that:

- the 5' primer is chosen from the SIL10 primer represented by the following sequence SEQ ID NO: 10:

5' GTTGCTGGAAGGAAGAACAGGATGGATCTG 3'

or any sequence derived from this sequence SEQ ID NO: 10, in particular by suppression and/or substitution and/or addition of one or more nucleotides, said derived sequence being hybridized, like the sequence SEQ ID NO: 10, with all or part of the nucleotide sequence complementary to the nucleotide sequences delimited by the nucleotides situated in positions 9 and 38 of the sequences SEQ ID NO: 1, 3, and 5,

- the 3' primer is chosen from the SIL8 primer represented by the following sequence SEQ ID NO: 11:

5' CAGTCCCAAGTGCCTGAACACACATGCACC 3'

or any sequence derived from this sequence SEQ ID NO: 11, in particular by suppression and/or substitution and/or addition of one or more nucleotides, said derived sequence being hybridized, like the sequence SEQ ID NO: 11, with all or part of the nucleotide sequences delimited by the nucleotides situated in positions 276 and 302 of the sequences SEQ ID NO: 1, 3, and by the nucleotides situated in positions 273 and 299, of the sequence SEQ ID NO: 5.

29. (currently amended) A nucleotide sequence characterized ~~in that it~~, wherein said nucleotide corresponds to the bovine *SI* gene represented by SEQ ID NO:1, or to the following fragments of the *SI* gene:

- any fragment chosen from those of approximately 10 to 300 nucleotides containing the nucleotides situated in positions 82 to 93 of the sequence SEQ ID NO: 1,

- the fragment SEQ ID NO: 7 of 294 nucleotides delimited by the nucleotides situated in positions 9 and 302 of the sequence SEQ ID NO: 1.

30. (currently amended) A nucleotide sequence ~~characterized in that it~~ wherein said nucleotide sequence corresponds to the bovine *si* gene represented by SEQ ID NO: 3, or to the following fragments of the *si* gene:

- any fragment chosen from those of approximately 10 to 300 nucleotides containing the nucleotides situated in positions 82 to 93 of the sequence SEQ ID NO: 3,

- the fragment SEQ ID NO: 8 of 294 nucleotides delimited by the nucleotides situated in positions 9 and 302 of the sequence SEQ ID NO: 3.

31. (currently amended) A nucleotide sequence ~~characterized in that it~~ wherein said nucleotide sequence

corresponds to the bovine *si*$_1$ gene represented by SEQ ID NO: 5, or to the following fragments of the *si*$_1$ gene:

- any fragment chosen from those of approximately 10 to 300 nucleotides containing the nucleotides situated in positions 82 to 93 of the sequence SEQ ID NO: 5,

- the fragment SEQ ID NO: 9 of 291 nucleotides delimited by the nucleotides situated in positions 9 and 299 of the sequence SEQ ID NO: 5.

32. (currently amended) A nucleotide sequence ~~characterized in that it~~ wherein said nucleotide sequence comprises:

- the SIL10 nucleotide sequence represented by the following sequence

SEQ ID NO: 10:

' GTTGCTGGAAGGAAGAACAGGATGGATCTG 3'

or any sequence derived from this sequence SEQ ID NO: 10, in particular by suppression and/or substitution and/or addition of one or more nucleotides, said derived sequence being hybridized, like the sequence SEQ ID NO: 10, with all or part of the nucleotide sequence complementary to the nucleotide sequences delimited by the nucleotides situated in positions 9 and 38 of the sequences SEQ ID NO: 1, 3, and 5,

- the SIL8 nucleotide sequence represented by the following sequence

SEQ ID NO: 11:

5' CAGTCCCAAGTGCCTGAACACACATGCACC 3'

or any sequence derived from this sequence SEQ ID NO: 11, in particular by suppression and/or substitution and/or addition of one or more nucleotides, said derived sequence being hybridized, like the sequence SEQ ID NO: 11, with all or part of the nucleotide sequences delimited by the nucleotides situated in positions 276 and 302 of the sequences SEQ ID NO: 1, 3, and by the nucleotides situated in positions 273 and 299, of the sequence SEQ ID NO: 5.

33. (currently amended) A Primer ~~pairs~~ pair, wherein each of the two primers ~~comprising~~ comprise, independently of one other, approximately 10 to approximately 30 nucleotides, ~~characterized in that they~~ wherein said primers are chosen in such a manner that one of the two sequences of ~~a~~ the primer pair is hybridized with a sequence of approximately 10 to approximately 30 nucleotides comprised in the nucleotide sequence complementary to the sequence delimited by the nucleotides situated in positions 1 and approximately 60 of the nucleotide sequences SEQ ID NO: 1, 3, and 5, whilst the other sequence of this same pair is hybridized with a sequence of approximately 10 to approximately 30 nucleotides comprised between the nucleotide situated in position 94 and the last of the nucleotides of the sequences SEQ ID NO: 1, 3, and 5.

34. (currently amended) The ~~Primer pairs~~ primer pair for gene amplification according to claim 33, ~~characterized in that~~ wherein:

- one of the primers is chosen from the sequences comprising the SIL10 sequence represented by SEQ ID NO: 10, or any sequence derived from this sequence SEQ ID NO: 10, in particular by suppression and/or substitution and/or addition of one or more nucleotides, said derived sequence being hybridized, like the sequence SEQ ID NO: 10, with all or part of the nucleotide sequence complementary to the nucleotide sequences delimited by the nucleotides situated in positions 9 and 38 of the sequences SEQ ID NO: 1, 3, and 5,

said primer being advantageously labelled, in particular in a radioactive or fluorescent manner,

- whilst the other primer is chosen from the sequences comprising the SIL8 sequence represented by SEQ ID NO: 11, or any sequence derived from this sequence SEQ ID NO: 11, in particular by suppression and/or substitution and/or addition of one or more nucleotides, said derived sequence being hybridized, like the sequence SEQ ID NO: 11, with all or part of the nucleotide sequences delimited by the nucleotides situated in positions 276 and 302 of the sequences SEQ ID NO: 1, 3, and by the nucleotides situated in positions 273 and 299, of the sequence SEQ ID NO: 5.

35. (currently amended) A method for the identification of populations or breeds of ruminant mammals such as cattle, sheep and goats, said method being carried out starting with a biological sample collected from the animal, in particular starting with sperm, embryo, blood, milk, hairs, carcass or meat, or other products derived from the latter, and making it possible to check, or even to certify, whether or not the animal from which said biological sample was collected belongs to a population or breed of ruminant mammals, this method comprising:

- a stage of amplification of the number of copies of the different allelic forms of the *SILVER* gene, namely of the *SI*, and/or *si*, and/or si_1 alleles, and/or of fragments of these allelic forms, specific to a population or breed of specific ruminant mammals, and capable of being present in said biological sample,

- a stage of detection of said allelic forms or fragments of the latter,

~~characterized in that~~ wherein the stage of amplification of the number of copies of the different allelic forms of the *SILVER* gene, or of the fragments of these allelic forms, is carried out using a primer pair as defined in claim 33.

36. (currently amended) A method for the identification of populations or breeds of ruminant mammals such as cattle, sheep and goats, said method being carried out starting with a

biological sample collected from the animal, in particular starting with sperm, embryo, blood, milk, hairs, carcass or meat, or other products derived from the latter, and making it possible to check, or even to certify, whether or not the animal from which said biological sample was collected belongs to a population or breed of ruminant mammals, this method comprising:

- a stage of amplification of the number of copies of the different allelic forms of the *SILVER* gene, namely of the *SI*, and/or *si*, and/or si_1 alleles, and/or of fragments of these allelic forms, specific to a population or breed of specific ruminant mammals, and capable of being present in said biological sample,

- a stage of detection of said allelic forms or fragments of the latter,

~~characterized in that~~ wherein the stage of amplification of the number of copies of the different allelic forms of the *SILVER* gene, or of the fragments of these allelic forms, is carried out using a primer pair as defined in claim 33,

said method being characterized in that:

- the detection of a genotype comprising the *si* allele in the biological sample studied ~~makes it possible~~ is able to certify that said sample originates from an animal belonging to the Charolais breed or having at least one ancestor of the Charolais breed,

- the detection of a genotype comprising the si_1 allele in the biological sample studied makes it possible to certify that said sample originates from an animal belonging to the Simmental breed or having at least one ancestor of the Simmental breed,

- the detection of a genotype comprising the *SI* allele, makes it possible to certify that said sample does not originate from an animal of the Charolais breed.

37. (currently amended) A kit for the implementation of a method according to claim 20, ~~characterized in that it~~ wherein said kit comprises at least one primer pair wherein each of the two primers comprising, independently of one other, approximately 10 to approximately 30 nucleotides, ~~characterized in that they~~ wherein said primers are chosen in such a manner that one of the two sequences of a primer pair is hybridized with a sequence of approximately 10 to approximately 30 nucleotides comprised in the nucleotide sequence complementary to the sequence delimited by the nucleotides situated in positions 1 and approximately 60 of the nucleotide sequences SEQ ID NO: 1, 3, and 5, whilst the other sequence of this same pair is hybridized with a sequence of approximately 10 to approximately 30 nucleotides comprised between the nucleotide situated in position 94 and the last of the nucleotides of the sequences SEQ ID NO: 1, 3, and 5, and if appropriate the reagents necessary for the implementation of the

amplification reaction of the number of copies of the different allelic forms of the *SILVER* gene.

38. (new) An isolated nucleotide sequence comprising the nucleotides 82-93 of SEQ ID NO: 3.

39. (new) The isolated nucleotide sequence according to claim 38, wherein said sequence comprises nucleotides 9-302 of SEQ ID NO: 3.

40. (new) The isolated nucleotide sequence according to claim 38, wherein said sequence comprises the nucleotides of SEQ ID NO: 3.

41. (new) The isolated nucleotide sequence according to claim 38, wherein said nucleotide sequence consists of the nucleotides 82-93 of SEQ ID NO: 3.

42. (new) The isolated nucleotide sequence according to claim 38, wherein nucleotide sequence consists of the nucleotides 9-302 of SEQ ID NO: 3.

43. (new) The isolated nucleotide sequence according to claim 38, wherein said nucleotide sequence consists of the nucleotides of SEQ ID NO: 3.